

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/564,266  
Source: IFWP  
Date Processed by STIC: 2/7/07

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IFWP

## RAW SEQUENCE LISTING

DATE: 02/07/2007

PATENT APPLICATION: US/10/564,266

TIME: 10:03:55

Input Set : A:\40184-5.APP

Output Set: N:\CRF4\02072007\J564266.raw

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3 <110> APPLICANT: Yang, Hongyuan
4     National University of Singapore
6 <120> TITLE OF INVENTION: Triacylglycerol-Deficient Fission Yeast and Its Uses
8 <130> FILE REFERENCE: 040184-000500US
10 <140> CURRENT APPLICATION NUMBER: US 10/564,266
11 <141> CURRENT FILING DATE: 2006-01-09
13 <150> PRIOR APPLICATION NUMBER: US 60/485,385
14 <151> PRIOR FILING DATE: 2003-07-09
16 <150> PRIOR APPLICATION NUMBER: WO PCT/SG04/00205
17 <151> PRIOR FILING DATE: 2004-07-09
19 <160> NUMBER OF SEQ ID NOS: 24
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 25
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
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29 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
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37 <211> LENGTH: 28
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39 <213> ORGANISM: Artificial Sequence
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42 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
43     amplification primer PLH1-53
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49 <210> SEQ ID NO: 3
50 <211> LENGTH: 28
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
56     amplification primer PLH1-35
58 <400> SEQUENCE: 3
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62 <210> SEQ ID NO: 4
63 <211> LENGTH: 27
64 <212> TYPE: DNA
65 <213> ORGANISM: Artificial Sequence

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67 <220> FEATURE:
68 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
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75 <210> SEQ ID NO: 5
76 <211> LENGTH: 26
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78 <213> ORGANISM: Artificial Sequence
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84 ggggtaccga atccatgggt agtgat                26
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 27
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:primer DG11-53
95 <400> SEQUENCE: 6
96 ccgctcgagc ccgttctata taatcgt                27
99 <210> SEQ ID NO: 7
100 <211> LENGTH: 27
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
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112 <211> LENGTH: 29
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence:primer DGA1-33
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120 gctctagact gaatgaatat tagtaacgc            29
123 <210> SEQ ID NO: 9
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125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
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130     amplification primer pca15
132 <400> SEQUENCE: 9
133 ataagaatgc ggccgcggaa gaactttgac acgtt      35
136 <210> SEQ ID NO: 10
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138 <212> TYPE: DNA

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163 <211> LENGTH: 28
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
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171 <400> SEQUENCE: 12
172 ccgctcgagg gtaggtagta tagttaga                28
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176 <211> LENGTH: 19
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Description of Artificial Sequence:diagnostic PCR
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184 <400> SEQUENCE: 13
185 gagaaagaat gctgagtag                19
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189 <211> LENGTH: 18
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence:diagnostic PCR
195     primer in coding region of his3+
197 <400> SEQUENCE: 14
198 gagtctttaa ttcattac                18
201 <210> SEQ ID NO: 15
202 <211> LENGTH: 19
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of Artificial Sequence:diagnostic PCR
208     primer in region outside of flanking fragment of

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218 <213> ORGANISM: Artificial Sequence
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221 <223> OTHER INFORMATION: Description of Artificial Sequence:diagnostic PCR
222      primer in region outside of flanking fragment of
223      plhl+
225 <400> SEQUENCE: 16
226 gtatattagt attgcctaat                      20
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231 <212> TYPE: DNA
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234 <220> FEATURE:
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239 acgcgtcgac catggcgtct tcccaagaag a        31
242 <210> SEQ ID NO: 18
243 <211> LENGTH: 30
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence:RT-PCR primer
249      PLH3
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252 tcccccggggt taatttctag gtttatcgag        30
255 <210> SEQ ID NO: 19
256 <211> LENGTH: 29
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
262      amplification primer DGA1-5
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269 <211> LENGTH: 28
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
275      amplification primer DGA1-3
277 <400> SEQUENCE: 20
278 tcccccggggt taggctgaca acttcaat          28

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281 <210> SEQ ID NO: 21
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287 <223> OTHER INFORMATION: Description of Artificial Sequence:E. coli genomic
288     DNA PCR amplification primer DGK5
290 <400> SEQUENCE: 21
291 ggaattccat atggccaata ataccactg
294 <210> SEQ ID NO: 22
295 <211> LENGTH: 28
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence:E. coli genomic
301     DNA PCR amplification primer DGK3
303 <400> SEQUENCE: 22
304 tcccccggt tatccaaat gcgaccat
307 <210> SEQ ID NO: 23
308 <211> LENGTH: 345
309 <212> TYPE: PRT
310 <213> ORGANISM: Schizosaccharomyces pombe
312 <220> FEATURE:
313 <223> OTHER INFORMATION: diacylglycerol O-acyltransferase (dgal; GeneDB
314     Accession No. SPCC1235.15)
316 <400> SEQUENCE: 23
317 Met Ser Glu Glu Thr Ser Ile Pro Gly Ile Ile Ala Ser Thr Pro Pro
318   1           5           10           15
320 Ile Ser Lys Asp Ser Arg Arg Asn Val Ser His Trp Leu Gln Ala Leu
321           20           25           30
323 Ala Val Phe Leu His Ser Val Ser Leu Thr Leu Thr Ala Ser Trp Tyr
324           35           40           45
326 Thr Val Leu Trp Ala Phe Leu Pro Phe Trp Pro Phe Leu Ile Val Tyr
327           50           55           60
329 Leu Ile Trp Leu Ile Tyr Asp Asp Gly Phe Val Thr Gly Lys Asp Arg
330           65           70           75           80
332 Gln Lys Arg Trp Leu Arg Asn Ala Pro Pro Tyr Arg Trp Phe Cys His
333           85           90           95
335 Tyr Phe Pro Ile Arg Leu His Lys Thr Thr Glu Leu Asp Ser Glu Lys
336           100          105          110
338 Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Ile Ser Leu Gly Ala
339           115          120          125
341 Phe Gly Gly Phe Ala Ser Glu Gly Ala Asp Phe Ser Lys Leu Phe Pro
342           130          135          140
344 Gly Ile Asn Val Ser Val Leu Thr Leu Asn Ser Asn Phe Tyr Val Pro
345           145          150          155          160
347 Val Tyr Arg Asp Tyr Leu Met Ala Leu Asn Ile Asn Ser Val Ser Lys
348           165          170          175
350 Lys Ser Cys Val Ser Ile Leu Ser Arg Lys Pro Gly Asp Ser Val Leu

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VERIFICATION SUMMARY

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